

# **FIGURE 1**

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
GTTGAAGGGTGTCCCCCTAAATGTAATACCTCCTCATCTTCTTACACAGTG  
TCTGAGAACATTACATTAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA  
CTACTCTTCTGACAGTCAGACTGGTCTCTACACTAAGACACCATGAAGGAGTATGTG  
CTCCTATTATTCTGGCTTGTGCTCTGCCAACCCCTCTTAGCCCTCACACATCGCACT  
GAAGAACATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAACGCCATTTC  
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGCTATTACAGAGTTGACATTGCTC  
AGATTTAGGTTGACCTCAGTCCCACCAACATTCCATTGATACTCGAATGCTGATCTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTAAAGGACTCACTCACTTATGGT  
CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTAACACAAAGAA  
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAACGTAAAGTAAACCACTTAATCTTCC  
CATTAGCAGAACTCAGAATTGATGAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA  
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAATGGGATAGA  
GCCAGGGCATTGAAGGGTGACGGTGTCCATATCAGAATTGCGAGAACACTGACCT  
CAGTTCTAAAGGCTTACCAACTTATTGGAGCTTCACCTAGATTATAAAATTCA  
ACAGTGGAACTTGAGGATTTAAACGATAAAAGAAACTACAAAGGCTGGCCTAGGAAACAA  
CAAATCACAGATATCGAAAATGGGAGTCTGCTAACATACCACGTGAGAGAAATACATT  
TGGAAAACAATAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACTCCAGATA  
ATCTTCCCTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTATACAGTGAATAAGTTATTCAACAAACCGGTGAAATACTGGG  
AAATGCAACCTGCAACATTGTTGTGTTGAGCAGAATGAGTGTTCAGCTGGAACTTT  
GGAATGTAATAATTAGTAATTGTAATGTCATTAAATATAAGATTCAAATCCCTACATT  
TGGAAACTTGAACTCTATTAAATGGTAGTTATATAACAGCAAATATCTATTCTCA  
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAAATTGCGAAACTATT  
GATACATAAGGGTTGAGAGAAACAAGCATCTATTGAGCTTCTTGTGACAAATGAT  
CTTACATAAAATCTCATGCTGACCATTCTTCTTCATAACAAAAAGTAAGATATTGGTA  
TTAACACTTGTATCAAGCACATTAAAAAGAACTGTACTGTAATGGAATGCTTGACT  
TAGCAAAATTGCTCTTCATTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTATTCTTAGTAACCTGGTAGTACTGTAATATTAAAT  
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTGTGACT  
CTTATGTTAAAACATAATTCTTAAATAAGCCTCAGTAAATGTTCTTACCAACTTGA  
TAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT  
ACCTGATTAAAATCTGTAAAAACGTGAGTGTGTTCATAAAATCTGTAACCTGCATT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC  
TTCAACTCTAAGGAATATTGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA  
CACTAACATTCTACACCAATTGCTCTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA  
TATAATGCTCAGAGTTCTTATGTATTGCTTATTGGCATTCAACATATGAAAATCAGAAA  
ACAGGGAAAATTTCATTAAAATATTGGTTGAAAT

## FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pi: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR  
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL  
KYLQIIIFLHSNSIARGVVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

**Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

TOPPE30 "474541650

### **FIGURE 3**

CGGACGCGTGGCGGACGCGTGGGCCCGSGCACCGCCCCCGGCCCTCCGCCCTCCGACTCGCGCCTCC  
CTCCCCTCCGCCGCTCCCGCCCTCCCTCCCTCCCTCCCTCCAGCTGTCCCCTTCGCGTC**ATGCC**GAGCCCTCCC  
GGCCCCCGCCGGCCCCGCTGCTGCTCCCTCGGGCTGCTGCTCGCTCCGCCGGCCGCCGGCGCCGGCCAGA  
GCCCCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCGTTCCGGGAGCCGGCAGGCTGCACCTTCGGCGG  
GAAGGTCTATGCCTTGACGAGACGTCGGCACCCGACCTAGGGCAGCCATTGGGATGCGCTGCGTGTG  
CGCCTGCGAGGCGCTCAGTGGGTCCCGTACCAAGGGCCCTGGCAGGTCAGCTGCAAGAACATCAAACAGA  
GTGCCAACCCCCGGCTGTGGCAGCCGAGCTGCCGGACACTGCTGCCAGACCTGCCAGCCCCAGGAGCGCAG  
CAGTCGGAGCGGCAGCCAGCGGCCCTGCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTAGCGACCG  
CGGGGAGCCAGGGCTGAGGAGCGGGCCGTTGACGCCACACGGACTTCGTTGCGCTGACAGGGCGAG  
GTCGCAAGGCGGTGGCACGAGCCGAGTCTCGCTGCGCTCTAGCCTCGCTCTATCTCCTACAGCGGCT  
GGACCGCCCTACCAGGATCCGTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGCAGCCCCCACCA  
AGATGGCCTGGTCTGTGGGTGTGGCGGGCAGTGCCTCGGGTGTCTCGGGCTCTAGGGCAGAACAGCTGCA  
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGGCTGC  
AGAGACCTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCTAGGGGATCACCCCTGCTCACTCT  
CAGTGCACACAGAGGACTCCTGCAATTGGCTGCTCTCCGAGGGCTGCTGGAACCCAGGAGTGGGACTAAC  
CCAGGTTCCCTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCAATGTCAGCCCA  
GGAACCAGGCTTGCTGAGGTGCTGCCAACCTGACAGTCAGGAGATGGACTGGCTGGTGTGGGAGCTGCA  
GATGGCCCTGGAGTGGCAGGCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT  
CCTGCAAAGTGTCTTGCTGGGCTGATGCCCTGATCCCAGTCAGACGGGTGCTGCCGCTCAGCCAGCCTCAC  
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCATGACACT  
GGAGACCAAGCCTCAGCGGAGGGATCAGCGACTGCTCTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC  
GGCGTGGGTATCTGCCCTGGCTGGTGCCAGGGCTCATATGCTGCTGCGAATGAGCTTCTGAACGT  
GGGCACCAAGGACTCCCAGACGGAGAGCTCGGGGCACGGCTGCCCTGCCACTGTGGCATAGCGCCCG  
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCAAGCAGCAGGGCACGC  
CTGGCTTCCCTGGATACCCACTGTCACCTGCACTATGAAGTGCTGCTGGCTGGCTGGCTCAGAACAGG  
CACTGTCACTGCCACCTCTGGCTGGCCTCTGGAACGCCAGGGCTCGCGGCTGCTGAAAGGGATTCTATGGCTC  
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGAAGTGTGCGGCACCTGGAAAAGGCATGGCTCCCTGAT  
GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCCGAGGGCAGGTGACATAGCCAACCAATGTGAGGTGGCGG  
ACTGCGCCTGGAGGCGGGGGCCGAGGGGGTGCAGGGCTGGGCTCCGGATACAGCCTCTGCTGCGCCGCC  
TGTGGTGCCTGGTCTCCGGCCCTAGCGCCGCCAAACCTGGTGTCTGGGCCGGCCAGACCCAAACACATG  
CTTCTCGAGGGGAGCGAGGCCACGGGCTCGCTGGCGCCAAACTACGACCCGCTGCTCACTCTGCA  
CTGCCAGAGACGAACGGTGTACCGTGCACCCGGTGTGCCCCACGCCAGCTGCCACACCCGGTGAGGCTCC  
CGACCAAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCAGGGCTGCCAGAGGCCGGACCC  
AGGAGAGGGCTGCTATTGTGACGGAGCTGGCGGGAGCGGGTACGGCTGGCACCCGGTTGTGCCCC  
CTTGGCTTAATTAAAGTGTGCTGTCACCTGCAAGGGGGCACTGGAGAGGTGACTGTGAGAACGGTGCAGTG  
TCCCCGGCTGGCTGTGCCAGCCTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGTCGGG  
GCCCAACCCAGCTGGGGACCCATGCAGGCTGATGGGCCCGGGCTGCCCTTGCTGGCAGTGGTCCC  
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCTTGAGAGATGAGCTGTATCACCTGAGATGTGGGGCAGG  
GGTGCCTCACTGTGAGGGATGACTGTCAGTGCCTGCTGGCTGGGAAGGAGAGTCGATGCTGTT  
CCGCTGCACGGCCCACGGCGCCCCAGAGACAGAGACTGATCCAGAGCTGGAGAAAGAACGCCAGGCTCTT**A**  
**GGGAGCAGCCAGAGGGCAAGTGCACCAAGAGGATGGGGCTGAGCTGGGAAGGGGTGGCATCGAGGACCTT**  
GCATTCTCCTGTGGGAAGCCAGTGCCTTGCTCCTCTGCTCGCTACTCCACCCCACTACCTCTGGAA  
CCACAGCTCCACAAGGGGGAGAGGCCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAAGTCTGCCCTGCCACCC  
TCGGCCTCTGTCTGGAAAGCCCACCCCTTCTCTGTACATAATGTCAGTGCTGTTGGATTTTAATT  
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG  
TTTGTATTAAAAACATTCTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 4**

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLGLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE  
TWHPDLGQPFGVMRVCVLCAEAPQWGRRTRGPGRVSCKNIKPECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVAR  
ARVSLLRSSLRFSISYRRLDRPTRIRFSDNSGSVLFEPAAPTQDGLVCGVWRAPRLSLRL  
LRAEQLHVALVTLTHPSGEVGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTVQEMD  
WLVLGELQMALEWAGRPGRLISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
GSЛИYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGKDFPDGELRGHVAALPYCGHSARHDTPVPLAGALVLPPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGLRLEAAGAEGVRALGAPDTASAAPPVV  
PGLPALAPAKPGGGPGRPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC  
PPSCPQVQADQCCPVCPEKQDVRDLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCCKQCPVGSAGHPQLGDPMQADG  
PRGCRFAGQWFPEQSWSHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGKESRCCS  
RCTAHRRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

## **FIGURE 5**

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGTCACTGCG  
TCCTGGCTCCGGCTCCCGGCCCTCCGGGCCAGTGCAGCCCCGCCGCCAGGGCGCCGGTGCAGCTGC  
TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGAGCGGGGCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG  
CCCGGCCCTTGTCTGCGCCGGCGTGCAGCCCTGCCGAATGGGGGTGTGCACTCGGCCCTG  
AGCCGGACCCGCAGCACCCGGCCCCGCCGGAGGCCTGGCTACAGCTGCACCTGCCCGCCGGATCTCCGGCG  
CCAAGTGCAGCTTGTGAGATCCTTGCCAGCAACCCCTGTCACCATGGCAACTGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGCTATGAAGGTCCAACGTGAAACAGGCACCTCCAGTC  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCTGACA  
AAATCCTGCTCGCTCAGGCAACGGTACACTGCTCACCTGGCAGCCAAAACAGGGCAGAAAGTTGAGAAA  
TGAAATGGATCAAGTGGAGGTGATCCCAGATATTGCCCTGTGGAATGCCAGTTAACAGCTCTGGGGTG  
GCCTGGTATCCTTGAAAGTGCCACAGAACACCTCAGTCAAGATTGGCAAGATGCCACTGCCTCACTGATTG  
TCTGGAAGGTCACGGCCACAGGATTCAAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT  
CAGGGGACTGGTCTCTGGAGGAGATGCTCGCCTGGGAATAATCACTTATTGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTGCGCTTAACCTCTGGTGTGAAGGTCAAGCACCTGTGTGCCGGGGAGAGTCACG  
CAAATGACTGGAGTTCAGGAAAAGGAAAATGCACACAGAACGGTCAAGAGGAACTTTCTGTACCTGTG  
AGGAGCAGTACGTGGTACTTCTGTGAAGAACATCGATGCTTGCCAGAGGAAACCTGCCAAAACAACCGAGCT  
GTATTGATGCAAATGAAAGCAAGATGGAGCAATTTCACCTGTGTTGCCCTGGTTAACTGGAGAGCTT  
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGAACTTCGGATCTGCTTGAAAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT  
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCCAGGCTTCACAGGGCGA  
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGGACCAGCT  
ACAAATGCCCTGTGATCCAGGTACCATGCCCTACTGTGAGGAGGAATAATGAGTGCCTCTCCGCTCCAT  
GCCCTGAATGCAGCCACCTGCAGGGACCTGTTAATGGCTATGAGTGTGTCCTGCCAGAATAACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCACTGTCTGAAACGGAGCCACCTGTGACAGCGACGGCCTGA  
ATGGCACGTGCATCTGTGACCCGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC  
CCTGCCACCATGGTGGAGCTGCCCTGGACAGCCAAATGGTTATAACTGCCACTGCCGATGGTGGGGAG  
CAAACGTGAGATCCACCTCCAATGGAAGTCCGGCACATGGCGAGAGCCTACCAACATGCCACGGACTCCC  
TCTACATCATCATTGGAGCCCTGCGTGGCCTTCATCCTATGCTGATCATCCTGATCGTGGGGATTGCCGCA  
TCAGCCGCATTGAATACCAGGGTCTTCCAGGCCAGCCTATGAGGAGTTACAACGTGCCGACATCGACAGCG  
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTGAAAGAAATCCGGCTGCAATGTATGATGTGA  
GCCCATGCCCTATGAAGATTACAGTCCGTGACAAACCTGGTCACACTGATTAAGAAACTAAAGATTGTAAT  
CTTTTTGGATTATTTCAAAAGATGAGATACTACACTCATTAAATATTTAAGAAAATAAGCTTAA  
GAAATTAAAATGCTAGCTCAAGAGTTCACTGAGTAAATTTAAGAACTAATTCTGCAAGCTTTAGTTG  
AAAAAAATTTAAAAACAAAATTGTGAAACCTATAGACGATTTAATGTACCTTCAGCTCTAAACTGT  
GTGCTCTACTAGTGTGCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTGTTACA  
GAATAAGTCAATCAAGGAGAAGTTCTGTGTTGACGTTGAGTGCCTGTTCTGAGTAGAGTTAGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATACCGTTACTAAAAAGAAGTCTGAAATGTTGTTG  
AGAAAAGTAAATTACTATCCCTAACCGAATGAAATTAGCCTTGCCATTCTGTGCAAGGGTAAGTAAC  
TTATTCTGCACTGTTGTTGAACTTGTGAAACATTCTTCAGTTGAGTTGTTGTCATTCTGTAACAGTCG  
TCGAACTAGGCCTCAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGATTAATCTATATT  
TTCTTAAAAAGTCAGGGTTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTGTTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTCCCTCAGTAGTGAGTATTCTCATAGTGCAAGCTTATTATCTCCAGGATGTT  
TTTGTGGCTGTATTGATTGATATGTGCTCTTGCAATTCCAACCATTGAATAATGTGATC  
AAGTCA

## **FIGURE 6**

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALLLLLLGGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCCEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGEELCQSKIDYCILDPCRNGATCISSLSGFTQCPEGYFGSACEEKVDPC  
ASSPCQNNGTCYVDGVHFTNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAELYKGTHTCELYKDPCANVSCLNGATC  
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDPNGYNCHCPHWVGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFY  
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## **FIGURE 7**

CTCTGGAAGGTACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGACTGGCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGCGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACCTGTGTTGCCTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACGTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 8**

CTCTGGAAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTCAGGCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA  
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC  
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC  
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACCTGTGTTGCCTCC  
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAG

## **FIGURE 9**

GCTGAGTCTGCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCTGCAAGAGCAGGCACGGCCCT  
GATGCGGGACTTCCCGCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTCTAGCTACGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGCCCTCGTGGCGCCAGTTCTGGTCAGCCTATGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCCCTCACCCGGAGCAGATTGACCTCATGCCGATGTGCCT  
CCTATTCTGAGCTGGAGCTTGACCTCGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA  
GCTCCGCTAACGGCGTCCACTCCTCTACAACAAACATCAGCGGCTGACTGACTTTGGTAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCACTCGCTGCC  
GGGGTGTGTGCAAACAGTGCTCGGAATGTTCTGATGACATCCTGAGCTTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTGCCATGGAGTAATAACAGTCAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGCCGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC  
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC  
TCGTGGAAACCTGCTCGGGCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCCCTGCCACTCCGACCTC  
TCACGTCTCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCCATA  
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCAGATGGCCCCAG  
TCCTTGCAGTTGTGGCACCTCCAGTCCTTATTCTGTGGCTCTTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA  
AATATTTCTGAAATAATGTTTGGACATAG

## **FIGURE 10**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595.  
<subunit 1 of 1, 433 aa, 1 stop  
<MW: 47787, pI: 6.11, NX(S/T): 5  
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNGGVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQS PLEDKF PDEQLSSS  
CHSDL SRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPVLILWL
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**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

## FIGURE 11

AAAACCTATAATATTCCGGATTATTACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTGACCCACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCGCTGTGGACGGCCAC  
AACGACCTGCCCTGGTCCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTCATGCCGCATGTGCTCCTATTCTGAGCTGGAGCTTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTCTACATGCTGGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGGTCCACTCCTTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCATGG  
GAGTAATACTGCAACCCATCAGCCAATGTGTCCTGTGGCAGATCACTTCGACCACATC  
AAGGCTGTATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGCCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGGTCTTCAGACAA  
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAAGTTCCCGGATGA  
GCAGCTGAGCAGTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCCTCCCCCACCCTGACAAAACTCACACATGCCACCGTGCCAGCACCTGA  
ACTCCTGGGGGACCGTCAGTCTCCTCTCCCCAAAACCCAAGGACACC

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSLEDKFPDEQLSSS
CHSDLRSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPDKTHTCPPCPAPELLGGP
SVFLFPPPKPKDT
```

## FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC  
CTGCGCCACCGCCGCCGAGCCGCAGCCCGCCGCCGCGCCCCCGGCAGCGCCGGCCCC**ATG**CCC  
GCCGGCCGCCGGGGCCCCGCCAATCCGCGCGGCCGCCGCGCCGTTGCTGCCCTGCT  
GCTGCTGCTCTGCGTCCTCGGGGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA  
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCCTAACGGCGCCGCTGCC  
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGCCCTGCCAACCTCAATGGGT  
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC  
TCCTGCCTCTATGTTGGCCTGCCCTAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACCA  
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGCCCGTGGGGCTGGAG  
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTCCCTTTCAAGCAA  
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTCGTCAAGTGC  
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCCTCCACTCCCCGAGCTGAGCCGGGGCCGGCGGCGGGCGTGCACCGC  
GGGGCGGAGAGCCGAGCTGGGGCCGGTGCAGCGAGCTCAAGCAGTCCCTGGCTGGCTC  
AAGAAGCACCGTACTGCTCCAACCTCAGCTTCCGCTCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA  
CGCGAGAGGTCTGCCAGA**TAAG**CTGTAGGGCTCAGGCCACCCCTCCCTGCCACGTGGAGA  
CGCAGAGGCCAACCAAACGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC  
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT  
GAGGCCACCTTGGGTGCACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC  
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC  
CCTCCAAAAGAGTCCTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

## **FIGURE 14**

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSQSARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLPPELSRLVNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRTPGAHGETFLHTNYSLKYLWRWYQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRGSARSDVLTLDILDVVTTDPPPDVHVSRVGG  
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSDWKVVDDVSNQTSCRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

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**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 44-61

**N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

**N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

**Amidation site.**

amino acids 3-7, 79-83, 411-415

**Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

## **FIGURE 15**

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAGGGATGAAATTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCAAGGTTACACTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGGCAG  
CTGGACATGTCTCGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACACTGGCTGCCTACAAATAACTGGAGTCAAAACACATG  
TCTGTGTCTAATTCGTAAACACTGGCTTACCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT  
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAAGCACCTAGTTCTGAAACACTGATTACCACTGGTGTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA  
TCATTGGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA  
ATTGTACCAACCGTTATTAAACATATATTATTATTGATTGACTAAATTGTTG  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA  
TGAAGGACTATCTAGGGTATTCAACATGAATATCATGAACCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCCAATGCCAAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pi: 9.52, NX(S/T): 1

MKFLLDILLPLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHVSVFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 170-187

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

**N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 17

GA C T A G T T C T C T T G G A G T C T G G G A G G A G G A A A G C G G A G C C G G C A G G G A G C G A A C C A G G A C T G  
G G G T G A C G G C A G G G C A G G G G G C C T G G C C G G G G A G A A G C G C G G G G C T G G A G C A C C A C C A A  
C T G G A G G G T C C G G A G T A G C G A G C G C C C G A A G G A G G C C A T C G G G A G C C G G A G G G G G A C T  
G C G A G A G G A C C C C G G C T C C G G C T C C C G G T G C C A G C G C T A G G C A G G C C A C T C C T C G T C C T G C  
T G C T C C T G G G C T G G C G G C G G C T G C C C C C A C T G G A C G A C A A C A A G A T C C C A G C C T C T G C  
C C G G G G C A C C C C G G C T T C C A G G C A C G C C G G G C C A C C A T G G C A G C C A G G G C T T G C C G G G C G  
C G A T G G C C G C G A C G G C C G C G A C G G C G C C C G G G C T C C G G G A G A G A A A G G C G A G G G C G G G A  
G G C C G G G A C T G C C G G G A C C T C G A G G G G A C C C C G G G C C G C G A G G A G A G G C G G G A C C C G C G G G G  
C C C A C C G G G C T G C C G G G G A G T G C T C G G T G C C T C C G C G A T C C G C C T T C A G C G C C A A G C G C T C  
C G A G A G C C G G G T G C C T C C G C G T C T G A C G C A C C C T G C C C T T C G A C C G C G T G C T G G T G A A C G  
A G C A G G G A C A T T A C G A C G C C G T C A C C G G C A A G T T C A C C T G C C A G G T G C C T G G G G T C T A C T A C  
T T C G C C G T C C A T G C C A C C G T C T A C C G G G C C A G C C T G C A G T T G A T C T G G T G A A G A A T G G C G A  
A T C C A T T G C C T C T T C T T C A G T T T T C G G G G G T G G C C C A A G C C A G C C T C G C T C T C G G G G G  
G G G C C A T G G T G A G G C T G G A G C C T G A G G A C C A A G T G T G G G T G C A G G T G G G T G T G G G T G A C T A C  
A T T G G C A T C T A T G C C A G C A T C A A G A C A G A C A G C A C C T T C T C C G G A T T T C T G G T G A C T C C G A  
C T G G C A C A G C T C C C C A G T C T T G C T T **T A G T** G C C C A C T G C A A A G T G A G C T C A T G C T C T C A C T C C  
T A G A A G G A G G G T G T G A G G C T G A C A A C C A G G T C A T C C A G G A G G G C T G G C C C C C T G G A A T A T T  
G T G A A T G A C T A G G G A G G T G G G G T A G A G C A C T C T C C G T C C T G C T G C T G G C A A G G A A T G G G A A C  
A G T G G C T G T C T G C G A T C A G G T C T G G C A G C A T G G G G C A G T G G C T G G A T T T C T G C C C A A G A C C A  
G A G G A G T G T G C T G T G C T G G C A A G T G T A A G T C C C C A G T T G C T C T G G T C C A G G A G C C C A C G G T  
G G G G T G C T C T C T C C T G G T C C T G C T T C T G G A T C C T C C C C A C C C C C T C C T G C T C C T G G G  
G C C G G C C C T T T C T C A G A G A T C A C T C A A T A A A C C T A A G A A C C C T C A T A A A A A A A A A A A A A A  
A A A A A A A A A A A A

DRAFT - NOT FOR CITATION

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLLLLGLAAGSPPILDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

## FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTG  
GCACCACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTCTTGCTCCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG  
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGGAGGAGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTGTCTGCGCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTGCTCGCA  
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTCTGTGAGGCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTG  
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGTGACATCGGCTACGGGGAGCCCAG  
TGTGCCACCAAGGTGCATTTCCCTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAGGCG  
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAAGGACATCCTGCCCTATCTGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGCT  
CACCTACAAGACGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACAGGCCCTCACCA  
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCCTCAACTGGAACGACCAGCGCTGAAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT  
GAGGCCTGACCACATGGCTCCCTGCCCTGGGAGCAGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA  
CCTTGACAAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGATTGGGAAGATGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCCAGAC  
CCTGTGGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pi: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLLHNRRLRSWV  
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG  
NWEVNGKTII PYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH  
CHCPCPGYTGRYCVRCSLQCVHGRFREEECSVCDIGYGGACATKVHFPFHTCDLRIDGDC  
FMVSSEADTYYRARMKCQRKGGLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG  
LYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMFGNCVELQASAANWNDQRCK  
TRNRYICQFAQEHISRWPGBS

**Signal sequence.**

amino acids 1-26

**Transmembrane domain.**

amino acids 110-124

**N-glycosylation sites.**

amino acids 144-148, 243-247

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

**N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

**EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

**C-type lectin domain signature.**

amino acids 417-442

## FIGURE 21

CGGACGCCGTGGCTGGCGCTGCAAAGCGTGTCCCAGCCGGTCCCCGAGCGTCCCCCGCCCGA  
CGCCCCGCCATGCTCCTGCTGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGA  
GGAAGAGGCGCAGAGCTGGGCCACTCTCGAGCAGGATGGACTCAGGGTCCCAGGCAAG  
TCAGACTGTTGAGAGGCTGAAAACCAAACCTTGTATGACAGAATTCTCAGTGAAGTCTACC  
ATCATTTCCCGTTATGCCTTCACTACGGTTCTGCAGAAATGCTGAACAGAGCTCTGAAGA  
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCAGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG  
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG  
AGCTTCTGCAGTGATTCCCAGCAAGGACAAGCCGCTTTCTGAGTTATGAGGAGCTTC  
TGCAGAGGCGCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGCCAGCAGCTGTCCGGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC  
GCTTCACAACACAGCAGGAGAGGGCAGTGGCGCGGGAAAGATGATTCTGGCCTCCCCCAT  
CTACTGTCACTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA  
AAGACCTCCTCCTTACCCAAGAATGTGGTATTGTGCTTGACAGCAGTGCTTATGGTG  
GGAACCAAACCCGGCAGACCAAGGATGCCCTTCACAATTCTCCATGACCTCCGACCCCA  
GGACCGTTCACTATGGATTTCACCGGATCAAAGTATGGAAGGACCACTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTACCATATGTCACCCACTGGA  
GGCACAGACATCAACGGGCCCTGCAGAGGGCCATCAGGCTCTCAACAAGTACGTGGCCA  
CAGTGGCATTGGAGACCGAGCGTGTCCCTCATCGTCTTGACGGATGGGAAGGCCACGG  
TCGGGGAGACGCACACCTCAAGATCCTCAACAAACACCGAGAGGCCGAGGGCAAGTC  
TGCATCTCACCATTGGCATGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTGCGCT  
GGAGAACTGTGGCCTCACACGGCGTGCACGAGGAGGACGAGGCTCGCAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCGCTCCTCTGACATCCGATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCCAACTACTTCAACGGCTGGAGATCATCAT  
TGCAGGGAAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA  
GTAAGAAATTCTCATCCTGAAGACAGATGTGCCTGTGGCCCTCAGAAGGCAGGAAAGAT  
GTCACAGGAAGCCCCAGGCCTGGAGGGCAGGGAGAGGGGACACCAACACATCGAGCGTCT  
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGAACGATGAACCGG  
AGAAGGAGCGGCTCGGGCAGCAGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTACTCCC  
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG  
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTCAGAGCGTGCAGGGAGCTGGCACGCAGC  
CAGGACCTTGCTCAAGAAGCCAAACTCCGTAAAAAAACAAAAACAAACAAAAAGA  
CATGGAGAGATGGTTTCTCTCCACCACTGGGATAACGATGAGAAGATGCCACCT  
GCAAGCCAGGAAGACGCCCTCACCAAGACACCATGTCTGCTGGCACCTTGATCTGGACCTC  
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTTGTAAAGCTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, PI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMLNRASEDQDIEFQMGI PAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE  
KRKNKTTEENGEGKTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRSL  
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANI IFKPTVVQQAR  
IAQNGILGDFI IRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHЛИSVPDSIRDGKVIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG  
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR  
DGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGCCGGCGGCCCTCCCGGGCTCCGGCTCTGCTGTTGCTCTTCTCCGCCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGG  
GAGGTTGCGACCATCAGTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGACTACTGAA  
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGCAGCAGGTTCACT  
TGCTGAATTTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA  
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCAGACTATCAGGTGGTCAAA  
GGGAACACAGAGCTAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACATGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTAGATGACTTATCCTCTACAAGGCTTAACCCGGAAAGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACCTGGTGAGAGTCGATG  
ATGAAATGCCAACACGCCGTACTGTCTGGGCCAACCTGTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCTCCCACAACAACCACCA  
CCACCACCACCACCAACCACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGGCGGTGGTGGTGGTGGTGG  
GCTGTGCTTGCTCATCATTCTGGGCGCTATTTGCCAGACATAAAGGTACATACTCACTC  
ATGAAGCAAAGGAGCCGATGACGCAGCAGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATTAGATCAGCTTTGTGTTCAAT  
GAGGTGTCCAACTGGCCTATTTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, PI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPNRQTIFYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG  
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

## **FIGURE 25**

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCCGA  
CCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC  
CCGGGACAGAAGATGTGCTCCAGGGCTCCCTGCTGCTGCCGCTGCTCCTGCTACTGCCCT  
GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAAGCCAGCACAGACAGTCTTCT  
GCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC  
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGCCCTGCCGGCTGCA  
GCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGCCCTGCCCTGCCCTGCTGCTGG  
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGGCCGATCCTGGACACTGCCAACGTGGAG  
GCGCTGCCGCTGGCTGGTCTGGGCTGCAGCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
CAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCAGCTGCCAGCTGCC  
GCCTCCGGGCTGACGCCCTGCCGCTGGCCGAAACACCCGATTGCCAGCTGCC  
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGAACCTAACGCTGCC  
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCCGCTGCTGCCAGCTGCCGCAACC  
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTCACA  
CTGGCCAGCCCTGAGGAGACGCCACTTCCCAGCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGAACCGCAGCTTGCTGCCAGCCACCCACACAGCCACAGTGCCACCA  
CGAGGCCGTGGTGCAGGAGCCCACAGCCTGTCTAGCTTGCTCCTACCTGGCTTAGC  
CCCACAGCGCCGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC  
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGG  
GGACACGGCACCACTGGCGTGCTTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGC  
CAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCC  
GACCCCTGGCATCGAGCCGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCC  
AGGGGAGCTCGTGAGCTCAGGAGCCTCCGTCTCACCTATGCAACCTATGGCCCTGAT  
AAGCGGCTGGTACGCTGCGACTGCCCTGCCCTCGCTGAGTACACGGTACCCAGCTGCG  
GCCAACGCCACTTAACCGTCTGTCTAGCCTTGGGCCGGGGCTGCCGGAGGGCG  
AGGAGGCCTGCCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACC  
CAGGCCCGAGGGCAACCTGCCCTCATTGCCGCCCTGGCGGGTGCCTGGC  
CGCGCTGGCTGCCGGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTC  
CCCTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTGA  
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCCTGCCCTCCAGTCACCCCTCACGCAAAGC  
CCTACATCAGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCCGTGCCACACCAACGTAAGTTCTCAGTCCCAACCTGGGATGTGCGAGA  
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT  
CCGCCCTGCCCTCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGGGACCCCTGGGGCCAGTGAAGGAAG  
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCAGGCTGTGACTCTAGTCTTGGCCCCAGG  
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTGGAAACATGTTGCTTTAA  
AATATATATATTTATAAGAGATCCTTCCCATTATCTGGAAAGATGTTTCAAACTC  
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATATGAAGGCCTTGTAAAGAAAAA  
ATAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, PI: 7.24, NX(S/T): 3

MCSRVPLLPPLLLALGPGVQGCPSCGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIILDTANVEALRL  
AGLGLQQLDEGLFSRLRNLDLSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP  
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPPSTAPPTVGPVPQPQDCCPPSTCLNGGTCHLGTRHHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTPRPPRSLTIGIEPVSPTRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLAEYVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAVCVRGRAMAAAQDKGQVPGAGPLELEGVKVPLEP  
GPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

## **FIGURE 27**

GGCACTAGGACAACTTCTCCCTCTGCACCACTGCCGTACCCCTACCGCCCCGCCACC  
TCCTTGCTACCCACTCTGAAACCACAGCTGTTGCAGGGTCCCCAGCTCATGCCAGCCTC  
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTGGTTGAGTTGGGGCAGCTCTGGGGCCGGCTTGCTTGCC  
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAAACAGAAGAACAGCAGCACTCTGCCTGCACCTGGTCCCATTAAACGCCACCTCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGAGAGGCCTAC  
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTAGCCAGGTC  
CTGTTCAAGACGTGACTTCACCATGGGTCAAGGTGGTCTCGAGAAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCAGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTCTAAATTCCCCGG  
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACTGTTGATT  
GTGTTATAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAGGAGAGGAAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC  
CCCGTTCCCTCACTTTCCCTTTCAATTCCCACCCCTAGACTTGTGATTTACGGATATCTTG  
CTTCTGTTCCCCATGGAGCTCCG

## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T) : 2

MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQLSRREV  
SRLQGTGGPSQNGEKY PWQSLPEQSSDALEAWENGERSRKRRRAVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTVEMWQPALRRGRGLQAQGYGVR I QDAGVYLLYSQVLFQDVFTTMGQVVSREG  
OGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVI I PRARAKLNLSPHGTFLGFVKL

## Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

### Tyrosine kinase phosphorylation site.

amino acids 156-164

#### **N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

## amino acids 34-45

## FIGURE 29

CACTTCTCCCTCTTCCTTACTTCAAGAAACCGCGCTTCCGCTCTGGTCGCAGAGAC  
CTCGGAGACC CGGCCGGGAGACGGAGGTGCTGGGTGGGGGACCTGGCTGCTCGTA  
CCGCCCCCCCACCCTCCTCTGCACTGCCGTCTCCGAAGACCTTTCCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTTGCCGGGGAGA  
TGCTCTAGGGCGGGCGGGAGGAGCGGCCGGGACGGAGGGCCGGCAGGAAGATGGC  
TCCC GTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTGCCTTGCCCTGGCCTGGT  
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGGAGGGACTGAGGAGCTGC  
CGTCGCCCTCCGGACCATGCCAGAGGGCTGAAGAACACATGAAAAATACAGGCCAGTCAG  
GACCAGGGCTCCCTGCTTCCGGTCTGCGCTGCTGTGACCCGGTACCTCATGTACCC  
GGCGACCGCCGTGCCAGATCAACATCACTATCTGAAAGGGAGAAGGGTACCGCGGAG  
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCCACACTGGA  
CCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTT CGGTGGCCGGAGAACGCCATGCACAGCAACC ACTACTACAGACGGTATCTCG  
ACACGGAGTTCGTGAACCTCTACGACCACCTCACATGTTCACGGCAAGTTCTACTGCTAC  
GTGCCCGGCCTCTACTCTTCAGCCTCACAGTGACACCTGGAACCAAGAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTATCTGTTCGGCAGGTGGGACCCGAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGTACGCC  
TACAAGGGCAGACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG  
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCACCTCCCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTCCCCGATCCCTGGACTCCGACTC  
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGCGATCGGTGCTCC  
CAGATCCCGAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGCACCGC  
GAGAACCCCTGGGACCTTCCCGGCCCTCTGCACACATCCTCAAGTGACCCGCACGGC  
GAGACCGGGTGGCGCAGGGCGTCCAGGGTGGCAGCGGGCTCCAGTCTGGAAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAAGAGAGAGGCTTTCTAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGTCAAGGGAGGGCCGGGAGG  
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTGAGGGTAGGTGGACCC  
CTGACATCCCTGTGGCCTTGGCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTCGAGGT  
GATGGGGCTGGGCCAGGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCTGCTTGGC  
TCCAGGTTGGTAGAAGCAGCCAGGGCTCCTGACAGTGGCAGGGACCCCTGGTCCCCA  
GGCCTGCAGATGTTCTATGAGGGGCAGAGCTCCTGGTACATCCATGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGGCCCTGGGGGTGGTCTCCATGCCTGCCACCCCTGGCATCGGCT  
TTCTGTGCCGCCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCTTGGCTCTGTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGCTAACGCATACCGCTT  
CCACGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTACTGCCCT  
CATCCAGGCCTCTGACCACTGAGGCTGAGAGGGCTTTCTAGGCTCAGAGCAGGGAGAG  
CTGGAAGGGCTAGAAAGCTCCGCTTGTCTGTTCTCAGGCTCTGTGAGCCTCAGTCCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCAATCACCGTGTAGGATTCACTCTCAGGAGC  
TGGGTGGCAGGAGAGGAATAGCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCTCGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCCTCTCCCTCCCCCATCCCCCACCTGGTTTGACTAACCTG  
TTCCTCTCTGGGCCCTGGCTGCCGGATCTGGGTCCCTAAGTCCTCTCTTAAAGAACTT  
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCCGAAGCAGAGGCCACACTC  
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

## **FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMF TGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

## FIGURE 31

GGCGGAGCATCCGCTGCCGCTCGCCGAGACCCCCCGCGCGGATTGCCGGTCTTCCCAGCG  
GCGCAGAGACTGTCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTCTAAAGCAAACTAAGACCAGAGGAGGATTAT  
CCTTGACCTTGAAGACCAAAACTAAACTGAAATTAAAATGTTCTTCGGGGAGAACGGAG  
CTTGACTTACACTTGGTAATAATTGCTCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGAAATC  
AGAGGCAATGAGCCGTATATACTCAACTCAAGAAGACTGCATTAATTCTGCTGTTAAC  
AAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTCTGTCACGAGGAAGCCTGTCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGACCAGAAATTGCCAAG  
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGGCAATTTCACAAGCAGTCACTCCCC  
TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT  
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA  
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTCTCCA  
CATACCACCTCGGCTACTCCAAGGCCACCCTCTACCCACCAATGCTCAGTGACACC  
TTCTGGACTTCCAGCCACAGCTGCCACCACAGCTCCACCTGTAACCACGTCACTTCTC  
AGCCTCCCACGACCCCTCATTTCTACAGTTTACACGGGCTGCCACTACCTCAAGCAATG  
GCTACAACAGCAGTTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATACCGTTACAGAAATCTCAAACCTAAACTTGAACACAGGAAATGTGTATAACCTA  
CTGCACCTTCTATGTCAAATGTGGAGTCTCCACTATGAATAAAACTGCTCCTGGAAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC  
ATTGAAAAATGGCTCTTATCGGGCTCTGCTCTTGGTGTCTCTGGTGTAGAGGCT  
TCGTCTCCTGGTAGAAATCCTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
TATTGATCAATGGATCTATGTGGACATCTAAAGGATGGAACTCGGTGTCCTTAATTCTT  
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG  
TATTGAAAGACAGGAAATGCCCTCTGCTCTTCTTGGAGACAGAGTCT  
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTGGCTCTCACCGAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAACGATCTGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTGGTATTTAGTAGAGACGGGTTCACCATGTTGGTCAGGCTG  
GTCTCAAACCTGACCTAGTGATCCACCCCTCTGGCTCCAAAGTGCTGGATTACAGG  
CATGAGCCACACAGCTGGCCCCCTCTGTTATGTTGGTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGTAATTGGTAATCTGTCTCTAAATATTAGCTAAAACAAAGCTCT  
ATGTAAGTAATAAAAGTATAATTGCCATATAAAATTCAAACGGCTTTATGCAAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCAATTACATTCTGGTTCCAGATAAAATCAAC  
TGTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCTTAAAACATTATT  
CCAGATGTAGTTCTTCAATTAAATATTGAATAAAATCTTTGTTACTCAA

## **FIGURE 32**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKSLEDVVIDIQSSLKGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKASWEGREASPGSSSQGSV  
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYILINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

## **FIGURE 33**

CGGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGGTGGTCTTC  
GCCTCCTTGTGTGCCCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCCTATAGCATCCGCAGCAGCTGGGAGAGGCCTGCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAACAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAAATGTAACTGGGA  
ATGTGACAGCAACACGATTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAG  
TTTATTCAAGAGTGCTGCTCCAAATCCCTGCTCTCATGGTACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAACATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA  
TGAAATTCAAGGTCTAGCTGGTATTATTGCAGCAAAAGGCTGGAACTCCCTCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAACGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGCCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAACATCTTATTCTAAATCCAACA  
GCCCATTTGATGAGTATTGGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTATACCAAGTATTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAA

## **FIGURE 34**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

**Signal sequence.**

amino acids 1-20

09614574728340

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125